

SEQUENCE LISTING

<110> Wu, Guang-Jer

<120> Diagnostic for Metastatic Prostate Cancer

<130> 95-97

<140> US unassigned

<141> 2000-09-01

<150> US 60/076,664

<151> 1998-03-03

<150> PCT US99/04850

<151> 1999-03-02

<160> 16

<170> PatentIn Ver. 2.0

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<211> 1950

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1938)

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Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala

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cct gag ctg gtg gag gtg gaa gtc agc aca gcc ctt ctg aag tgc 144  
Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys

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gtc cac aag gag aag cgg acg ctc atc ttc cgt gtg cgc cag ggc cag 240  
Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln

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ggc cag agc gaa cct ggg gag tac gag cag cgg ctc agc ctc cag gac	85	90	95	288
Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp				
aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac gag cgc	100	105	110	336
Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg				
atc ttc ttg tgc cag ggc aag cgc cct cgg tcc cag gag tac cgc atc	115	120	125	384
Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile				
cag ctc cgc gtc tac aaa gct ccg gag gag cca aac atc cag gtc aac	130	135	140	432
Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn				
ccc ctg ggc atc cct gtg aac agt aag gag cct gag gag gtc gct acc	145	150	155	480
Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr				
tgt gta ggg agg aac ggg tac ccc att cct caa gtc atc tgg tac aag	165	170	175	528
Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys				
aat ggc cgg cct ctg aag gag gag aag aac cgg gtc cac att cag tcg	180	185	190	576
Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser				
tcc cag act gtg gag tcg agt ggt ttg tac acc ttg cag agt att ctg	195	200	205	624
Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu				
aag gca cag ctg gtt aaa gaa gac aaa gat gcc cag ttt tac tgt gag	210	215	220	672
Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu				
ctc aac tac cgg ctg ccc agt ggg aac cac atg aag gag tcc agg gaa	225	230	235	720
Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu				
gtc acc gtc cct gtt ttc tac ccg aca gaa aaa gtg tgg ctg gaa gtg	245	250	255	768
Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val				
gag ccc gtg gga atg ctg aag gaa ggg gac cgc gtg gaa atc agg tgt	260	265	270	816
Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys				
ttg gct gat ggc aac cct cca cca cac ttc agc atc agc aag cag aac	275	280	285	864
Leu Ala Asp Gly Asn Pro Pro His Phe Ser Ile Ser Lys Gln Asn				

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Pro Ser Thr Arg Glu Ala Glu Glu Thr Thr Asn Asp Asn Gly Val	
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Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys	
305 310 315 320	
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Gln Gly Leu Asp Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln	
325 330 335	
gaa cta ctg gtg aac tat gtg tct gac gtc cga gtg agt ccc gca gcc	1056
Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala	
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cct gag aga cag gaa ggc agc agc ctc acc ctg acc tgt gag gca gag	1104
Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu	
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agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca ggc cag	1152
Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Gly Gln	
370 375 380	
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Ala Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly	
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Leu Asn Arg Thr Gln Leu Val Asn Val Ala Ile Phe Gly Pro Pro Trp	
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Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu	
435 440 445	
aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc tcc tgg	1392
Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp	
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Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val	
465 470 475 480	
ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag aca ggt	1488
Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly	
485 490 495	

gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc acc agc atc ctc			1536
Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu			
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ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc aac aca			1584
Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr			
515	520	525	
acc act ggc ctc agc act tcc act gcc agt cct cat acc aga gcc aac			1632
Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn			
530	535	540	
agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg ggc gtg			1680
Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Ser Arg Gly Val			
545	550	555	560
gtc atc gtg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg ctg ggc			1728
Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly			
565	570	575	
gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc agg cgc			1776
Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg			
580	585	590	
tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag agc gaa ctt			1824
Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Ser Glu Leu			
595	600	605	
gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc ctc ctg			1872
Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu			
610	615	620	
cag ggc agc agc ggt gac agg gct ccg gga gac cag gga gag aaa			1920
Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys			
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Tyr Ile Asp Leu Arg His			
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Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser  
50 55 60

Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln  
65 70 75 80

Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp  
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Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg  
100 105 110

Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile  
115 120 125

Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn  
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Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr  
145 150 155 160

Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys  
165 170 175

Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser  
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Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu  
195 200 205

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Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu  
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Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu  
225 230 235 240

Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val  
245 250 255

Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys  
260 265 270

Leu Ala Asp Gly Asn Pro Pro His Phe Ser Ile Ser Lys Gln Asn  
275 280 285

Pro Ser Thr Arg Glu Ala Glu Glu Thr Thr Asn Asp Asn Gly Val  
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Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys  
305 310 315 320

Gln Gly Leu Asp Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln  
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Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala  
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Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu  
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Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Gly Gln  
370 375 380

Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu  
385 390 395 400

Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly  
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Leu Asn Arg Thr Gln Leu Val Asn Val Ala Ile Phe Gly Pro Pro Trp  
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Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu  
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450 455 460

Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val  
465 470 475 480

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Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly  
485 490 495

Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu  
500 505 510

Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr  
515 520 525

Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn  
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Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val  
545 550 555 560

Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly  
565 570 575

Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg  
580 585 590

Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Ser Glu Leu  
595 600 605

Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu  
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Tyr Ile Asp Leu Arg His  
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Cys Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln  
15 20 25 30

cct gcg cct gag ctg gtg gag gtg gaa gtg ggc agc aca gcc ctt ctg 145  
Pro Ala Pro Glu Leu Val Glu Val Gly Ser Thr Ala Leu Leu  
35 40 45

aag tgc ggc ctc tcc cag tcc caa ggc aac ctc agc cat gtc gac tgg 193  
Lys Cys Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp  
50 55 60

ttt tct gtc cac aag gag aag cgg acg ctc atc ttc cgt gtg cgc cag 241  
Phe Ser Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln  
65 70 75

ggc cag ggc cag agc gaa cct ggg gag tac gag cag cgg ctc agc ctc 289  
Gly Gln Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu  
80 85 90

cag gac aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac Gln Asp Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp 95 100 105 110	337
gag cgc atc ttc ttg tgc cag ggc aag cgc cct cgg tcc cag gag tac Glu Arg Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr 115 120 125	385
cgc atc cag ctc cgc gtc tac aaa gct ccg gag gag cca aac atc cag Arg Ile Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln 130 135 140	433
gtc aac ccc ctg ggc atc cct gtg aac agt aag gag cct gag gag gtc Val Asn Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val 145 150 155	481
gct acc tgt gta ggg agg aac ggg tac ccc att cct caa gtc atc tgg Ala Thr Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp 160 165 170	529
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Glu Cys Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu		
320	325	330
cca cag gaa cta ctg gtg aac tat gtg tct gac gtc cga gtg agt ccc		1057
Pro Gln Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro		
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gca gcc cct gag aga cag gaa ggc agc agc ctc acc ctg acc tgt gag		1105
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Ala Glu Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr		
370	375	380
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Asp Gln Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys		
385	390	395
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Arg Glu Ala Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile		
400	405	410
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415	420	425
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cct tgg atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg		1345
Pro Trp Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met		
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Val Leu Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile		
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465	470	475
cga gtc ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag		1489
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480	485	490
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Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser		
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510		

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gcc aac agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg Ala Asn Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg 545 550 555	1681
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agg cgc tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag acc Arg Arg Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr 595 600 605	1825
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Arg	Gly	Ala	Thr	Leu	Ala	Leu	Thr	Gln	Val	Thr	Pro	Gln	Asp	Glu	Arg
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Ile	Phe	Leu	Cys	Gln	Gly	Lys	Arg	Pro	Arg	Ser	Gln	Glu	Tyr	Arg	Ile
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Pro	Leu	Gly	Ile	Pro	Val	Asn	Ser	Lys	Glu	Pro	Glu	Glu	Val	Ala	Thr
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Ser	Gln	Thr	Val	Glu	Ser	Ser	Gly	Leu	Tyr	Thr	Leu	Gln	Ser	Ile	Leu
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Lys	Ala	Gln	Leu	Val	Lys	Glu	Asp	Lys	Asp	Ala	Gln	Phe	Tyr	Cys	Glu
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Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala  
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Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu  
355 360 365

Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln  
370 375 380

Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu  
385 390 395 400

Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly  
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Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro Pro Trp  
420 425 430

Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu  
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450 455 460

Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val  
465 470 475 480

Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly  
485 490 495

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500 505 510

Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr  
515 520 525

Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn  
530 535 540

Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val  
545 550 555 560

Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly  
565 570 575

Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg  
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Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr Glu Leu  
595 600 605

Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu  
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<223> Description of Artificial Sequence:HUMAN MUC18  
cDNA, AS MODIFIED TO FACILITATE CLONING

<400> 5  
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gtggaagtgg gcagcacagc cttctgaag tgccgcctct cccagtccta aggcaacctc 180  
agccatgtcg actggtttc tgtccacaag gagaagcgga cgctcatctt ccgtgtgcgc 240  
cagggccagg gccagagcga acctggggag tacgagcagc ggctcagcct ccaggacaga 300  
ggggctactc tggccctgac tcaagtccacc ccccaagacg agcgcatctt cttgtgccag 360  
ggcaagcgcc ctgcgtccca ggagtaccgc atccagctcc gctgtacaa agtccggag 420  
gagccaaaca tccaggtcaa ccccctggc atccctgtga acagtaagga gcctgaggag 480  
gtcgctacct gtgtagggag gaacgggtac cccattcctc aagtcatctg gtacaagaat 540  
ggccggcctc tgaaggagga gaagaaccgg gtccacattc agtcgtccca gactgtggag 600  
tcgagtgggt tgtacacctt gcagagtatt ctgaaggcac agctggtaa agaagacaaa 660  
gatgcccagt tttactgtga gctcaactac cggctgccc gtggaaacca catgaaggag 720  
tccagggaaat tcaccgtccc tgtttctac ccgacagaaa aagtgtggct ggaagtggag 780  
cccgtggaa tgctgaagga aggggaccgc gtggaaatca ggtgtttggc tcatggcaac 840  
cctccaccac acttcagcat cagcaagcag aaccccagca ccagggaggc agaggaagag 900

acaaccaacg acaacggggc cctggtgctg gagcctgccc ggaaggaaca cagtggcgc 960  
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ctactggtga actatgtgtc tgacgtccga gtgagtcgg cagccccctga gagacaggaa 1080  
ggcagcagcc tcaccctgac ctgtgaggca gagagtagcc aggacctcga gttccagtgg 1140  
ctgagagaag agacagacca ggtgctggaa agggggcctg tgcttcagtt gcatgacctg 1200  
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ccccggccca ccatotcctg gaacgtcaac ggcacggcaa gtgaacaaga ccaagatcca 1440  
cagcgagtcc tgagcaccct gaatgtcctc gtgaccccg agctgttgg aacaggtgtt 1500  
gaatgcacgg cctccaaacga cctgggcaaa aacaccagca tcctcttctt ggagctggc 1560  
aatttaacca ccctcacacc agactccaac acaaccactg gcctcagcac ttccactgcc 1620  
agtcctcata ccagagccaa cagcacctcc acagagagaa agctgccgga gccggagagc 1680  
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atcacgctgc ccccgctcg taagaccgaa cttgttagtt aagttaagtc agataagctc 1860  
ccagaagaga tgggcctcct gcagggcagc agcggtgaca agagggctcc gggagaccag 1920  
ggagagaaat acatcgatct gaaggcatta gccccgaatc at 1962

<210> 6  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial  
Sequence:OLIGONUCLEOTIDE, FOR SUBCLONING HUMAN  
MUC18 FRAGMENT

<400> 6  
ggatcccagc tggtaaaaga agacaaag

28

<210> 7

<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial  
Sequence:OLIGONUCLEOTIDE, FOR SUBCLONING HUMAN  
MUC18

<400> 7  
ctggaaactcg aggtcctggc tactctc

27

<210> 8  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:AMINO ACID  
SEQUENCE ENCODED BY PORTION OF PGEX-6P-1 VECTOR

<400> 8  
Gly Pro Leu Gly Ser  
1 5

<210> 9  
<211> 27  
<212> DNA  
<213> Artificial Sequence

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<220>  
<223> Description of Artificial  
Sequence:OLIGONUCLEOTIDE, SEQUENCE CORRESPONDS TO  
HUMAN MUC18

<400> 9  
ctcgggatcc atggggcttc ccaggct

27

<210> 10  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial  
Sequence:OLIGONUCLEOTIDE, SEQUENCE CORRESPONDS TO  
HUMAN MUC18

<400> 10

tcggggctaa tgcctcagat cgatg

25

<210> 11  
<211> 81  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:JUNCTION  
SEQUENCE FOR MCU18 CLONED INSERT

<400> 11  
ctggaaagttc tgttccaggg gcccctggga tccccggaaat tcccccgggtcg actcgagcgg 60  
ccgcacatcgatg actgactgac g 81

<210> 12  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:JUNCTION  
SEQUENCE FOR CLONED MUC18 INSERT

<400> 12  
Leu Glu Val Leu Phe Gln Gly Pro Leu Gly Ser Pro Glu Phe Pro Gly  
1 5 10 15

Arg Leu Glu Arg Pro His Arg Asp  
20

<210> 13  
<211> 81  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:JUNCTION  
SEQUENCE FOR CLONED MUC18 INSERT

<400> 13  
ctggaaagttc tgttccaggg gcccctggga tccccaggaa ttccccgggtcg gactcgagcgg 60  
ccgcacatcgatg actgactgac c 81

<210> 14  
<211> 23

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:JUNCTION  
SEQUENCE IN FUSION PROTEIN

<400> 14  
Leu Glu Val Leu Phe Gln Gly Pro Leu Gly Ser Pro Gly Ile Pro Gly  
1 5 10 15  
Ser Thr Arg Ala Ala Ala Ser  
20

<210> 15  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:JUNCTION  
SEQUENCE IN VECTOR WITH MCU18 CLONED INSERT  
  
<400> 15  
cttggaaagtcc tttttccaggg gcccctggga tccccgaatt cccgggtcga ctcgagcggc 60  
cgccatcgtga ctgactga 78

---

<210> 16  
<211> 25  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:JUNCTION OF  
FUSION PEPTIDE

<400> 16  
Leu Gly Val Leu Phe Gln Gly Pro Leu Gly Ser Pro Asn Ser Arg Val  
1 5 10 15  
Asp Ser Ser Gly Arg Ile Val Thr Asp  
20 25